

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 16, 2004, 07:46:14 / Search time 0.691275 Seconds
(without alignments)
0.145 Million cell updates/sec

Title: US-09-879-257A-1

Perfect score: 206
Sequence: 1 QTDMSRKAFVPPKESDTSYV.....WRALKYEVQGEVFTKPLMP 206

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 1 seqs, 486 residues

Word size : 6

Total number of hits satisfying chosen parameters: 0

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : rapb6.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Score	Match	Length	ID	Description
No matches found					

Search completed: December 16, 2004, 07:46:15
Job time : 0.691275 secs

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OM protein - protein search, using sw model

Run on: December 16, 2004, 07:47:32 ; Search time 0.001 Seconds
(without alignments)
200.232 Million cell updates/sec

Title: US-09-879-257A-1
Perfect score: 206
Sequence: 1 QTDMSRKAFYPPKESDTSY.....WRALKVEVGGEVFTKPOLMP 206

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 2 seqs, 972 residues

Word size : 6

Total number of hits satisfying chosen parameters: 0

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : rapm6.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description

No matches found

Search completed: December 16, 2004, 07:47:32
Job time : 0.001 secs

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OM protein - protein search, using sw model

Run on: December 16, 2004, 07:48:45 ; Search time 0.001 Seconds
(without alignments)
100.116 Million cell updates/sec

Title: US-09-879-257A-1

Perfect score: 206
Sequence: 1 QTDMSRKAFVPPKESDTSYV.....WRALKVEVGGEVFTKPLWP 206

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 1 seqs, 486 residues

Word size : 6

Total number of hits satisfying chosen parameters: 0

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : rpr6.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Score	Length	ID	Description

No matches found					

Search completed: December 16, 2004, 07:48:45
Job time : 0.001 secs

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OM protein - protein search, using sw model

Run on: December 16, 2004, 07:43:29 ; Search time 0.001 Seconds
(without alignments)
31.104 Million cell updates/sec

Title: US-09-879-257A-2
Perfect score: 16
Sequence: 1 DMSRKATVFYFKESDTS 16

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 4 seqs, 1944 residues

Word size : 6

Total number of hits satisfying chosen parameters: 0

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: listing first 45 summaries

Database : rag6.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result	Query			
No.	Score	Match	Length	ID
Description				
No matches found				

Search completed: December 16, 2004, 07:43:29
Job time : 0.001 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 16, 2004, 07:46:14 ; Search time 0.0536913 Seconds
(without alignments)
0.145 Million cell updates/sec

Title: US-09-879-257A-2

Perfect score: 16
Sequence: 1 DMSRKAFVFPKESDTS 16

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 1 seqs, 486 residues

Word size : 6

Total number of hits satisfying chosen parameters: 0

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database : rapb6.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result	Query			
No.	Score	Match	Length	ID
		DB	ID	Description

No matches found

Search completed: December 16, 2004, 07:46:15
Job time : 0.0536913 secs

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OM protein - protein search, using sw model

Run on: December 16, 2004, 07:47:32 ; Search time 0.001 Seconds
(without alignments)
15.552 Million cell updates/sec

Title: US-09-879-257A-2

Perfect score: 16

Sequence: 1 DMSRKAFVFPKESDTS 16

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 2 seqs, 972 residues

Word size : 6

Total number of hits satisfying chosen parameters: 0

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : rapm6.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description

No matches found

Search completed: December 16, 2004, 07:47:32
Job time : 0.001 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 16, 2004, 07:48:45 : Search time 0.001 Seconds
(without alignments)
7.776 Million cell updates/sec

Title: US-09-879-257A-2
Perfect score: 16
Sequence: 1 DMSRKAFVFPKESDTS 16

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 1 seqs, 486 residues

Word size : 6

Total number of hits satisfying chosen parameters: 0

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database : rpr6.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
No matches found					

Search completed: December 16, 2004, 07:48:45
Job time : 0.001 secs

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OM protein - protein search, using sw model

Run on: December 16, 2004, 07:43:29 ; Search time 0.001 Seconds
(without alignments)
52.488 Million cell updates/sec

Title: US-09-879-257A-3

Perfect score: 27
Sequence: 1 LVGDIGNVMWDFVLSPEINTIYLGG 27

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 4 seqs, 1944 residues

Word size : 6

Total number of hits satisfying chosen parameters: 0

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: listing first 45 summaries

Database : rag6.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description

No matches found

Search completed: December 16, 2004, 07:43:29
Job time : 0.001 secs

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OM protein - protein search, using sw model

Run on: December 16, 2004, 07:46:14 ; Search time 0.090604 Seconds
(without alignments)
0.145 Million cell updates/sec

Title: US-09-879-257A-3

Perfect score: 27

Sequence: 1 LVGDIGNVMWDFVLSPEINTIYLG 27

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 1 seqs, 486 residues

Word size : 6

Total number of hits satisfying chosen parameters: 0

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database : rapb6.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result	Query				
No.	Score	Match	Length	ID	Description

No matches found

Search completed: December 16, 2004, 07:46:15
Job time : 0.090604 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 16, 2004, 07:47:32 ; Search time 0.001 Seconds
(without alignments)
26.244 Million cell updates/sec

Title: US-09-879-257A-3
Perfect score: 27
Sequence: 1 LVGDIGNVMWDFVLSPDEINTIYLG 27

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 2 seqs, 972 residues

Word size : 6

Total number of hits satisfying chosen parameters: 0

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database : rapm6.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description

No matches found

Search completed: December 16, 2004, 07:47:32
Job time : 0.001 secs

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OM protein - protein search, using sw model

Run on: December 16, 2004, 07:48:45 ; Search time 0.001 Seconds
(without alignments)
13.122 Million cell updates/sec

Title: US-09-879-257A-3

Perfect score: 27
Sequence: 1 LVGDIGNVMWDFVLSPEINTIYLGG 27

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 1 seqe, 486 residues

Word size : 6

Total number of hits satisfying chosen parameters: 0

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : rpr6.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	ID	Description

No matches found			

Search completed: December 16, 2004, 07:48:46
Job time : 1 secs

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OM protein - protein search, using sw model

Run on: December 16, 2004, 07:43:29 ; Search time 0.001 Seconds
(without alignments)
23.328 Million cell updates/sec

Title: US-09-879-257A-46
Perfect score: 12
Sequence: 1 DPRVRGLYFPAG 12

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 4 seqs, 1944 residues

Word size : 6

Total number of hits satisfying chosen parameters: 0

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : rag6.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description

No matches found

Search completed: December 16, 2004, 07:43:29
Job time : 0.001 secs

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OM protein - protein search, using sw model

Run on: December 16, 2004, 07:46:14 : Search time 0.0402685 Seconds
(without alignments)
0.145 Million cell updates/sec

Title: US-09-879-257A-46
Perfect score: 12
Sequence: 1 DPRVRGLYFPAG 12

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 1 seqs, 486 residues

Word size : 6

Total number of hits satisfying chosen parameters: 0

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database : rapb6.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result	Query		
No.	Score	Match Length	ID

Description			

No matches found			

Search completed: December 16, 2004, 07:46:15
Job time : 0.0402685 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 16, 2004, 07:47:32 ; Search time 0.001 Seconds
(without alignments)
11.664 Million cell updates/sec

Title: US-09-879-257A-46
Perfect score: 12
Sequence: 1 DPRVRLGLYFPAG 12

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 2 seqs, 972 residues

Word size : 6

Total number of hits satisfying chosen parameters: 0

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : rapm6.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Score	Match	Length	ID	Description

No matches found

Search completed: December 16, 2004, 07:47:32
Job time : 0.001 secs

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OM protein - protein search, using sw model

Run on: December 16, 2004, 07:48:45 ; Search time 0.001 Seconds
(without alignments)
5.832 Million cell updates/sec

Title: US-09-879-257A-46
Perfect score: 12
Sequence: 1 DPRVRGLYFPAG 12

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 1 seqs, 486 residues

Word size : 6

Total number of hits satisfying chosen parameters: 0

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : rpr6.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Score	Match	Length	ID	Description
No matches found					

Search completed: December 16, 2004, 07:48:46
Job time : 0.001 secs

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OM protein - protein search, using sw model

Run on: December 16, 2004, 07:43:29 ; Search time 0.001 Seconds
(without alignments)
23.328 Million cell updates/sec

Title: US-09-879-257A-4
Perfect score: 12
Sequence: 1 LKKGTYGAEAS 12

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 4 seqs, 1944 residues

Word size : 6

Total number of hits satisfying chosen parameters: 0

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : rag6.ped:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Score	Match	Length	ID	Description

No matches found

Search completed: December 16, 2004, 07:43:29
Job time : 0.001 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 16, 2004, 07:46:14 ; Search time 0.0402685 Seconds
(without alignments)

0.145 Million cell updates/sec

Title: US-09-879-257A-4

Perfect score: 12

Sequence: 1 LKGGYTVGAFAAS 12

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 1 seqs, 486 residues

Word size : 6

Total number of hits satisfying chosen parameters: 0

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : rapb6.pdb:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	ID	Description
No matches found			

Search completed: December 16, 2004, 07:46:15
Job time : 0.0402685 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 16, 2004, 07:47:32 ; Search time 0.001 Seconds
(without alignments)
11.664 Million cell updates/sec

Title: US-09-879-257A-4
Perfect score: 12
Sequence: 1 LKKGYTVGAENS 12

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 2 seqs, 972 residues

Word size : 6

Total number of hits satisfying chosen parameters: 0

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : rapm6.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Score	Match	Length	ID	Description

No matches found					

Search completed: December 16, 2004, 07:47:32
Job time : 0.001 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 16, 2004, 07:48:45 : Search time 0.001 Seconds
(without alignments)
5.832 Million cell updates/sec

Title: US-09-879-257A-4
Perfect score: 12
Sequence: 1 LKKGYTVGAERS 12

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 1 seqe, 486 residues

Word size : 6

Total number of hits satisfying chosen parameters: 0

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: listing first 45 summaries

Database : rpr6.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	ID	Description
No matches found			

Search completed: December 16, 2004, 07:48:46
Job time : 0.001 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 16, 2004, 07:43:29 ; Search time 0.001 Seconds
(without alignments)
29.160 Million cell updates/sec

Title: US-09-879-257A-50
Perfect score: 15
Sequence: 1 ERVEWLRKQLQDVHN 15

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 4 seqs, 1944 residues

Word size : 6

Total number of hits satisfying chosen parameters: 0

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : rag6.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result	Query			
No.	Score	Match	Length	ID

Description				

No matches found

Search completed: December 16, 2004, 07:43:29
Job time : 0.001 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 16, 2004, 07:46:14 ; Search time 0.0503356 Seconds
(without alignments)
0.145 Million cell updates/sec

Title: US-09-879-257A-50
Perfect score: 15
Sequence: 1 ERVWMLRKXIQDVHN 15

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 1 seqs, 486 residues

Word size : 6

Total number of hits satisfying chosen parameters: 0

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : rapb6.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Score	Match	Length	ID	Description

No matches found

Search completed: December 16, 2004, 07:46:15
Job time : 0.0503356 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 16, 2004, 07:47:32 ; Search time 0.001 Seconds
(without alignments)
14.580 Million cell updates/sec

Title: US-09-879-257A-50
Perfect score: 15
Sequence: 1 ERVEMLRKXLDVHN 15

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 2 seqs, 972 residues

Word size : 6

Total number of hits satisfying chosen parameters: 0

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : rapm6.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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No matches found

Search completed: December 16, 2004, 07:47:32
Job time : 0.001 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 16, 2004, 07:48:45 ; Search time 0.001 Seconds
(without alignments)
7.290 Million cell updates/sec

Title: US-09-879-257A-50
Perfect score: 15
Sequence: 1 ERVEMLRKQLQDVHN 15

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 1 seqs, 486 residues

Word size : 6

Total number of hits satisfying chosen parameters: 0

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: listing first 45 summaries

Database : rpr6.pdb:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
No matches found					

Search completed: December 16, 2004, 07:48:46
Job time : 0.001 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 16, 2004, 07:43:29 : Search time 0.001 Seconds
(without alignments)
19.440 Million cell updates/sec

Title: US-09-879-257A-5
Perfect score: 10
Sequence: 1 RALKYVQGE 10

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 4 seqs, 1944 residues

Word size : 6

Total number of hits satisfying chosen parameters: 0

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : rag6.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description

No matches found

Search completed: December 16, 2004, 07:43:29
Job time : 0.001 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 16, 2004, 07:46:14 ; Search time 0.033557 Seconds
(without alignments)
0.145 Million cell updates/sec

Title: US-09-879-257A-5
Perfect score: 10
Sequence: 1 RALKYEVQGE 10

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 1 seqs, 486 residues

Word size : 6

Total number of hits satisfying chosen parameters: 0

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : rapb6.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description

No matches found

Search completed: December 16, 2004, 07:46:15
Job time : 0.033557 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 16, 2004, 07:47:32 ; Search time 0.001 Seconds
(without alignments)
9.720 Million cell updates/sec

Title: US-09-879-257A-5
Perfect score: 10
Sequence: 1 RALKYEVQGE 10

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 2 seqs, 972 residues

Word size : 6

Total number of hits satisfying chosen parameters: 0

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : rapm6.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
No matches found					

Search completed: December 16, 2004, 07:47:32
Job time : 0.001 secs

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OM protein - protein search, using sw model

Run on: December 16, 2004, 07:48:45 ; Search time 0.001 Seconds
(without alignments)
4.860 Million cell updates/sec

Title: US-09-879-257A-5
Perfect score: 10
Sequence: 1 RALKYEVQGE 10

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 1 seqs, 486 residues

Word size : 6

Total number of hits satisfying chosen parameters: 0

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : rpr6.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Score	Length	ID	Description
No matches found					

Search completed: December 16, 2004, 07:48:46
Job time : 0.001 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 14, 2004, 09:44:28 ; Search time 50 Seconds
(without alignments)
389.950 Million cell updates/sec

Title: US-09-879-257A-6_COPY_1_294
Perfect score: 1516
Sequence: 1 MVSEIKTLVFPFGTGLAK.....IYDAEYVKYFVRAQYGAGD 294

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 0

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 100%
Maximum Match 100%
Listing first 65000 summaries

Database : Issued Patente AA:*

1:	/cgn2_6/ptodata/1/1aa/5A_COMB.pep:*
2:	/cgn2_6/ptodata/1/1aa/5B_COMB.pep:*
3:	/cgn2_6/ptodata/1/1aa/6A_COMB.pep:*
4:	/cgn2_6/ptodata/1/1aa/6B_COMB.pep:*
5:	/cgn2_6/ptodata/1/1aa/PCTUS_COMB.pep:*
6:	/cgn2_6/ptodata/1/1aa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description

No matches found

Search completed: December 14, 2004, 09:55:15
Job time : 53 secs

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OM protein - protein search, using sw model

Run on: December 14, 2004, 09:53:14 ; Search time 164 Seconds
(without alignments)
640.307 Million cell updates/sec

Title: US-09-879-257A-6_COPY_1_294
Perfect score: 1516
Sequence: 1 MVSEIKTLVTFPGGTGLAKR.....IYDAEVNKKYFVRAQYGAGD 294

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1585576 seqs, 357178320 residues

Total number of hits satisfying chosen parameters: 1

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 100%
Maximum Match 100%
Listing first 65000 summaries

Database : Published Applications AA:*
1: /cgn2_6/ptodata/1/pubppa/US07_PUBSCOMB.pep:*
2: /cgn2_6/ptodata/1/pubppa/PCT_NEW_PUB.pep:*
3: /cgn2_6/ptodata/1/pubppa/US06_NEW_PUB.pep:*
4: /cgn2_6/ptodata/1/pubppa/US06_PUBSCOMB.pep:*
5: /cgn2_6/ptodata/1/pubppa/US07_NEW_PUB.pep:*
6: /cgn2_6/ptodata/1/pubppa/PCTUS_PUBSCOMB.pep:*
7: /cgn2_6/ptodata/1/pubppa/US08_NEW_PUB.pep:*
8: /cgn2_6/ptodata/1/pubppa/US08_PUBSCOMB.pep:*
9: /cgn2_6/ptodata/1/pubppa/US09_PUBSCOMB.pep:*
10: /cgn2_6/ptodata/1/pubppa/US09_PUBSCOMB.pep:*
11: /cgn2_6/ptodata/1/pubppa/US09C_PUBSCOMB.pep:*
12: /cgn2_6/ptodata/1/pubppa/US09_NEW_PUB.pep:*
13: /cgn2_6/ptodata/1/pubppa/US10_PUBSCOMB.pep:*
14: /cgn2_6/ptodata/1/pubppa/US10_PUBSCOMB.pep:*
15: /cgn2_6/ptodata/1/pubppa/US10C_PUBSCOMB.pep:*
16: /cgn2_6/ptodata/1/pubppa/US10_NEW_PUB.pep:*
17: /cgn2_6/ptodata/1/pubppa/US10_NEW_PUB.pep:*
18: /cgn2_6/ptodata/1/pubppa/US11_NEW_PUB.pep:*
19: /cgn2_6/ptodata/1/pubppa/US60_NEW_PUB.pep:*
20: /cgn2_6/ptodata/1/pubppa/US60_PUBSCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	1516	100.0	486 9 US-09-879-257A-6	Sequence 6, Appl1

ALIGNMENTS

RESULT 1
US-09-879-257A-6
; Sequence 6, Application US/09879257A
; Patent No. US20020081650A1
; GENERAL INFORMATION:
; APPLICANT: YAMAMOTO, SACHIKO
; APPLICANT: HANADA, TOSHIRO

; APPLICANT: SHIRO, MINORU
; APPLICANT: KOBATAKE, SHINZO
; TITLE OF INVENTION: HYBRID ENZYMES AND USE THEREOF
; FILE REFERENCE: 55986(70281)
; CURRENT APPLICATION NUMBER: US/09/879,257A
; CURRENT FILING DATE: 2001-06-12
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 486
; TYPE: PRT
; ORGANISM: Leuconostoc mesenteroides
US-09-879-257A-6

Query Match 100.0%; Score 1516; DB 9; Length 486;
Best Local Similarity 100.0%; Pred. No. 6.4e-127;
Matches 294; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MVSEIKTLVTFPGGTGLAKRKLPSVFNLYKKGYLQKHFALVGTARQALNDEFKQLV	60
DB	1	MVSEIKTLVTFPGGTGLAKRKLPSVFNLYKKGYLQKHFALVGTARQALNDEFKQLV	60
QY	61	DSIKDFTDDQAQAEAFIEHFSYRAHDVTDAASTAVLKEAIEADKPDIDGNRIFYNSVA	120
DB	61	DSIKDFTDDQAQAEAFIEHFSYRAHDVTDAASTAVLKEAIEADKPDIDGNRIFYNSVA	120
QY	121	PRFPGTIAXYKLSGSLADTGYNRLMTEKPGTSYDTRAELQNDLENAFDNQLFRIDHY	180
DB	121	PRFPGTIAXYKLSGSLADTGYNRLMTEKPGTSYDTRAELQNDLENAFDNQLFRIDHY	180
QY	181	LGEKMNQNIALLRGNPIFDAAMNKDYIKNVQVTLSEVLGVEERAGYVDTAGALLDMIN	240
DB	181	LGEKMNQNIALLRGNPIFDAAMNKDYIKNVQVTLSEVLGVEERAGYVDTAGALLDMIN	240
QY	241	HTMQIVGWLAMEKPESTTDKDIRAKQAAPNALKIYDABVNNKTFVRAQYGAGD	294
DB	241	HTMQIVGWLAMEKPESTTDKDIRAKQAAPNALKIYDABVNNKTFVRAQYGAGD	294

Search completed: December 14, 2004, 10:06:55
Job time : 166 secs

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OM protein - protein search, using sw model

Run on: December 14, 2004, 09:47:04 ; Search time 488 Seconds
(without alignments)
667.524 Million cell updates/sec

Title: US-09-879-257a-6_COPY_1_294
Perfect score: 1516
Sequence: 1 MVSIRKTLVTFPGGTGLAK.....IYDAEVNKYFVRAQYGAGD 294

Scoring table:
BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 6730630 seqs, 110798698 residues

Total number of hits satisfying chosen parameters: 2

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 100%
Listing first 65000 summaries

Database :

Pending Patents AA Main:*

1: /cgn2_6/ptodata/1/paa/PCITUS_COMB.pep:*
2: /cgn2_6/ptodata/1/paa/US06_COMB.pep:*
3: /cgn2_6/ptodata/1/paa/US07_COMB.pep:*
4: /cgn2_6/ptodata/1/paa/US08_COMB.pep:*
5: /cgn2_6/ptodata/1/paa/US09_COMB.pep:*
6: /cgn2_6/ptodata/1/paa/US09_COMB.pep:*
7: /cgn2_6/ptodata/1/paa/US09_COMB.pep:*
8: /cgn2_6/ptodata/1/paa/US09_COMB.pep:*
9: /cgn2_6/ptodata/1/paa/US09_COMB.pep:*
10: /cgn2_6/ptodata/1/paa/US09_COMB.pep:*
11: /cgn2_6/ptodata/1/paa/US09_COMB.pep:*
12: /cgn2_6/ptodata/1/paa/US09_COMB.pep:*
13: /cgn2_6/ptodata/1/paa/US09_COMB.pep:*
14: /cgn2_6/ptodata/1/paa/US09_COMB.pep:*
15: /cgn2_6/ptodata/1/paa/US09_COMB.pep:*
16: /cgn2_6/ptodata/1/paa/US09_COMB.pep:*
17: /cgn2_6/ptodata/1/paa/US09_COMB.pep:*
18: /cgn2_6/ptodata/1/paa/US09_COMB.pep:*
19: /cgn2_6/ptodata/1/paa/US09_COMB.pep:*
20: /cgn2_6/ptodata/1/paa/US09_COMB.pep:*
21: /cgn2_6/ptodata/1/paa/US09_COMB.pep:*
22: /cgn2_6/ptodata/1/paa/US09_COMB.pep:*
23: /cgn2_6/ptodata/1/paa/US09_COMB.pep:*
24: /cgn2_6/ptodata/1/paa/US09_COMB.pep:*
25: /cgn2_6/ptodata/1/paa/US09_COMB.pep:*
26: /cgn2_6/ptodata/1/paa/US09_COMB.pep:*
27: /cgn2_6/ptodata/1/paa/US09_COMB.pep:*
28: /cgn2_6/ptodata/1/paa/US09_COMB.pep:*
29: /cgn2_6/ptodata/1/paa/US09_COMB.pep:*
30: /cgn2_6/ptodata/1/paa/US09_COMB.pep:*
31: /cgn2_6/ptodata/1/paa/US09_COMB.pep:*
32: /cgn2_6/ptodata/1/paa/US09_COMB.pep:*
33: /cgn2_6/ptodata/1/paa/US09_COMB.pep:*
34: /cgn2_6/ptodata/1/paa/US09_COMB.pep:*
35: /cgn2_6/ptodata/1/paa/US09_COMB.pep:*
36: /cgn2_6/ptodata/1/paa/US09_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	1516	100.0	486	22	US-09-791-537-11271
2	1516	100.0	486	23	US-09-879-257a-6

ALIGNMENTS

RESULT 1
US-09-791-537-11271
; Sequence 11271, Application US/09791537
; GENERAL INFORMATION:
; APPLICANT: Bionomix, Inc.
; APPLICANT: Debe, Derek
; APPLICANT: Danzer, Joseph
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBERS
; TITLE OF INVENTION: METHODS OF USE THEREOF
; FILE REFERENCE: 261/210
; CURRENT APPLICATION NUMBER: US/09/791,537
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 153055
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 11271
; LENGTH: 486
; TYPE: PRT
; ORGANISM: Leuconostoc mesenteroides
US-09-791-537-11271

Query Match
Best Local Similarity 100.0%; Score 1516; DB 22; Length 486;
Matches 294; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MVSIRKTLVTFPGGTGLAKRKLPSYFNLYKKGYLQGFPAIVGTARQALNDFEKLVR 60
DB 1 MVSIRKTLVTFPGGTGLAKRKLPSYFNLYKKGYLQGFPAIVGTARQALNDFEKLVR 60
QY 61 DSITDFDDQAQAAFEHPSYRAHDVTDAASVAVLKEATLEADKPDIDNRIFFYMSVA 120
DB 61 DSITDFDDQAQAAFEHPSYRAHDVTDAASVAVLKEATLEADKPDIDNRIFFYMSVA 120
QY 121 PRFPGTIAKYKSGGLADTGYNRLMEKPGTSYDTPAELQNDLENAFDNDQFRIDHY 180
DB 121 PRFPGTIAKYKSGGLADTGYNRLMEKPGTSYDTPAELQNDLENAFDNDQFRIDHY 180
QY 181 LGKEMVQNIARLRFGNPIFDAWKKDYIKNVQVTLSEVLGYEBRAGYYDTAGALLDMIQN 240
DB 181 LGKEMVQNIARLRFGNPIFDAWKKDYIKNVQVTLSEVLGYEBRAGYYDTAGALLDMIQN 240
QY 241 HTWQIVGLMKEKESFTDKDIRAKNAAFNALKIYDAEVNKYFVRAQYGAGD 294
DB 241 HTWQIVGLMKEKESFTDKDIRAKNAAFNALKIYDAEVNKYFVRAQYGAGD 294

RESULT 2
US-09-879-257a-6
; Sequence 6, Application US/09879257A
; GENERAL INFORMATION:
; APPLICANT: YAMAMOTO, SACHIRO
; APPLICANT: HANADA, TOSHIRO
; APPLICANT: SHIRO, MINORU
; APPLICANT: KOBATAKE, SHINZO
; TITLE OF INVENTION: HYBRID ENZYMES AND USE THEREOF
; FILE REFERENCE: 55986(70281)
; CURRENT APPLICATION NUMBER: US/09/879,257A
; CURRENT FILING DATE: 2001-06-12
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 486
; TYPE: PRT
; ORGANISM: Leuconostoc mesenteroides

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OM protein - protein search, using sw model

Run on: December 14, 2004, 09:50:04 ; Search time 29 Seconds
(without alignments)
434.426 Million cell updates/sec

Title: US-09-879-257a-6_COPY_1_294
Perfect score: 1516
Sequence: 1 MVSEIKTLVFPFGSTGLAK.....IYDEAEVNVKVFVRAQYAGD 294

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 16218 seqs, 42851568 residues

Total number of hits satisfying chosen parameters: 0

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 100%
Maximum Match 100%
Listing first 65000 summaries

Database : Pending Patents AA New:*

- 1: /cgn2_6/ptodata/1/paa/PCT_NEW_COMB.pep:*
- 2: /cgn2_6/ptodata/1/paa/US06_NEW_COMB.pep:*
- 3: /cgn2_6/ptodata/1/paa/US07_NEW_COMB.pep:*
- 4: /cgn2_6/ptodata/1/paa/US08_NEW_COMB.pep:*
- 5: /cgn2_6/ptodata/1/paa/US09_NEW_COMB.pep:*
- 6: /cgn2_6/ptodata/1/paa/US10_NEW_COMB.pep:*
- 7: /cgn2_6/ptodata/1/paa/US11_NEW_COMB.pep:*
- 8: /cgn2_6/ptodata/1/paa/US60_NEW_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query	Score	Match	Length	ID	Description

No matches found

Search completed: December 14, 2004, 10:04:05
Job time : 32 secs

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OM protein - protein search, using sw model

Run on: December 14, 2004, 09:43:43 ; Search time 45 Seconds
(without alignments)
628.616 Million cell updates/sec

Title: US-09-879-257A-6_COPY_1_294
Perfect score: 1516
Sequence: 1 MVSEIKTLVTFPGGTGDLAKR.....IYDEAEVNYKVFVRAQYGAGD 294

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 1

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 100%
Maximum Match 100%
Listing first 65000 summaries

Database : PIR 79: *
1: pir1: *
2: pir2: *
3: pir3: *
4: pir4: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1516	100.0	486	1 A39864	glucose-6-phosphat

ALIGNMENTS

RESULT 1

A39864
glucose-6-phosphate 1-dehydrogenase (EC 1.1.1.49) - leuconostoc mesenteroides
C/Species: Leuconostoc mesenteroides
C/Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C/Accession: A39864; A29027
R/Lee, W.T.; Flynn, T.G.; Lyons, C.; Levy, H.R.
J. Biol. Chem. 266, 13028-13034, 1991
A/Title: Cloning of the gene and amino acid sequence for glucose 6-phosphate dehydrogenase
A/Reference number: A39864; MUID:91302321; PMID:2071589
A/Accession: A39864
A/Molecule type: DNA
A/Residues: 1-486 <LES>
A/Cross-references: UNIPROT:P11411; GB:M64446; NID:G149630; PTDN:AAA25265.1; PID:G149631
R/Bhadbhade, M.M.; Adams, M.J.; Flynn, T.G.; Levy, H.R.
FEBS Lett. 211, 243-246, 1987
A/Title: Sequence identity between a lysine-containing peptide from leuconostoc mesenteroides
A/Reference number: A29027; MUID:87105980; PMID:3100332
A/Accession: A29027
A/Molecule type: Protein
A/Residues: 147-153, 'H', 155, 'I', 157-164, 'P', 166-188 <BHA>
C/Superfamily: glucose-6-phosphate dehydrogenase

C:Keywords: oxidoreductase; pentose phosphate pathway

Query Match 100.0%; Score 1516; DB 1; Length 486;
Best Local Similarity 100.0%; Pred. No. 1.5e-100;
Matches 294; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MVSEIKTLVTFPGGTGDLAKRKLPSVFNLYKKGYLQGHFAIVGTARQALNDDEFKQLYR	60
Db	1	MVSEIKTLVTFPGGTGDLAKRKLPSVFNLYKKGYLQGHFAIVGTARQALNDDEFKQLYR	60
Qy	61	DSIKDFTDDQQAQAEAFIEHESYRAHDVTDAAASYVLKEAIEBAADKFDIDGNRIIFYMSVA	120
Db	61	DSIKDFTDDQQAQAEAFIEHESYRAHDVTDAAASYVLKEAIEBAADKFDIDGNRIIFYMSVA	120
Qy	121	PRFPGTIATKYIKSGGLADTGYNRLMEKPGTGYDTPAAELQNDLENAFDONQLEFRIDHY	180
Db	121	PRFPGTIATKYIKSGGLADTGYNRLMEKPGTGYDTPAAELQNDLENAFDONQLEFRIDHY	180
Qy	181	LGEKMNQINIALRFGNPIFDAAWNRKDYIKNVQVTLSEVLGVEERAGYDRTAGALLDMIQN	240
Db	181	LGEKMNQINIALRFGNPIFDAAWNRKDYIKNVQVTLSEVLGVEERAGYDRTAGALLDMIQN	240
Qy	241	HTWQIVGWLAMEKESFTDKDIRAAKNAAFNALKIYDEAEVNYKVFVRAQYGAGD	294
Db	241	HTWQIVGWLAMEKESFTDKDIRAAKNAAFNALKIYDEAEVNYKVFVRAQYGAGD	294

Search completed: December 14, 2004, 09:54:19
Job time : 48 secs

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OM protein - protein search, using sw model

Run on: December 14, 2004, 09:43:03 ; Search time 206 Seconds
(without alignments)
821.166 Million cell updates/sec

Title: US-09-879-257a-6_COPY_1_294
Perfect score: 1516
Sequence: 1 MVSRIKTLVTFPGGTGLAK.....IYDEAEVKKYFVRAGYAGD 294

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 0

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 100%
Maximum Match 100%
Listing first 65000 summaries

Database : UniProt 02: *
1: uniprot_sprot: *
2: uniprot_trembl: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Score	Length	ID	Description

No matches found

Search completed: December 14, 2004, 09:53:27
Job time : 209 secs

GenCore version 5.1.6
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OM protein - protein search, using SW model

Run on: December 14, 2004, 09:39:47, Search time 171 Seconds
(without alignment)
616.763 Million cell updates/sec

Title: US-09-879-257a-6_COPY_1_294
Perfect score: 1516
Sequence: 1 MWSIKITLVTFPGGTGLAK.....IYDAENVKVFVRAQYAGD 294

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 4

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 100%
Maximum Match 100%
Listing first 65000 summaries

Database: 1: Geneseqp23Sep04:*
2: geneseqp19908:*
3: geneseqp20008:*
4: geneseqp20018:*
5: geneseqp20028:*
6: geneseqp20038:*
7: geneseqp20038:*
8: geneseqp20048:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1516	100.0	486	4 AAB74045	AAB74045 L. pseudo
2	1516	100.0	486	4 AAB74044	AAB74044 L. pseudo
3	1516	100.0	486	4 AAB74041	AAB74041 Leuconost
4	1516	100.0	486	5 AAB21112	AAB21112 Leuconost

ALIGNMENTS

RESULT 1
AAB74045
ID AAB74045 standard; protein; 486 AA.
XX
AC AAB74045;
XX
DT 15-JUN-2001 (first entry)
XX
XX L. pseudomesenteroides glucose-6-phosphate dehydrogenase mutant #4.
XX
XX Glucose-6-phosphate dehydrogenase; site-directed mutagenesis;
XX
XX enzyme stability; mutant; mutagen.
XX
XX Leuconostoc pseudomesenteroides.
XX
XX Synthetic.

PH Key Location/Qualifiers
FT Misc-difference 337 /note= "wild-type Ser substituted by Ala"
XX
XX
XX JP2001037480-A.
XX
XX
XX 13-FEB-2001.
XX
XX
XX 28-JUL-1999; 99JP-00213427.
XX
XX
XX 28-JUL-1999; 99JP-00213427.
XX
XX
XX (TOMY) TOYOBO KK.
XX
XX WPI; 2001-285598/30.
XX
XX

Mutant glucose-6-phosphate dehydrogenase and its preparation.
Example 1; Page; 15pp; Japanese.

The present sequence is one of nine mutants of the glucose-6-phosphate dehydrogenase from Leuconostoc pseudomesenteroides which were synthesized by site-directed mutagenesis. Primers were used to mutate the sequence of the wild-type glucose-6-phosphate dehydrogenase gene within the recombinant plasmid pG6D66 to produce plasmids pG6D66M1 and pG6D66M9. The present sequence is encoded by recombinant plasmid pG6D66M4. The stability of the mutant enzymes in liquid state is improved compared to the wild-type enzyme. The disclosed method is useful for the preparation of a mutant glucose-6-phosphate dehydrogenase of high purity in large quantities. Note: The present sequence is not shown in the specification but is derived from the Leuconostoc pseudomesenteroides wild-type glucose-6-phosphate dehydrogenase sequence shown in AAB74041

Sequence 486 AA;

Query Match 100.0%; Score 1516; DB 4; Length 486;
Best Local Similarity 100.0%; Pred. No. 7.7e-131;
Matches 294; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MWSIKITLVTFPGGTGLAKRLKLYPSVFNLYKKGYLQKHFAIVGTARQALNDFKQLVR	60
DB	1	MWSIKITLVTFPGGTGLAKRLKLYPSVFNLYKKGYLQKHFAIVGTARQALNDFKQLVR	60
QY	61	DSIKRPTDDQAQAEFIEHFSYRAVDYDAAYAVLAKENIEBAAXPDIDGNRIPTMSYA	120
DB	61	DSIKRPTDDQAQAEFIEHFSYRAVDYDAAYAVLAKENIEBAAXPDIDGNRIPTMSYA	120
QY	121	PRPFGTIKYLKSEGLADVTGYNRLMIKPFSTSYDTAAELQNDLENAPDDNQLEFRIDHY	180
DB	121	PRPFGTIKYLKSEGLADVTGYNRLMIKPFSTSYDTAAELQNDLENAPDDNQLEFRIDHY	180
QY	181	LGEKENVONIAALRFGNPIEDAAWNRDVIKNVQVTLSSEVLGVERAGYVDTAGALLDMIGN	240
DB	181	LGEKENVONIAALRFGNPIEDAAWNRDVIKNVQVTLSSEVLGVERAGYVDTAGALLDMIGN	240
QY	241	HTMOIVGWLAMEKPESTFDKDIRAKNAAPNALKTYDEENVKVFVRAQYAGD	294
DB	241	HTMOIVGWLAMEKPESTFDKDIRAKNAAPNALKTYDEENVKVFVRAQYAGD	294

RESULT 2
AAB74044
ID AAB74044 standard; protein; 486 AA.
XX
AC AAB74044;
XX
DT 15-JUN-2001 (first entry)
XX
XX L. pseudomesenteroides glucose-6-phosphate dehydrogenase mutant #3.
XX
XX Glucose-6-phosphate dehydrogenase; site-directed mutagenesis;
XX
XX enzyme stability; mutant; mutagen.
XX
XX

XX OS Leucostoc mesenteroides.
 XX FN EPI182213-A1.
 XX PD 27-FEB-2002.
 XX PF 08-JUN-2001; 2001EP-00113996.
 XX PR 12-JUN-2000; 2000JP-00174604.
 XX PR 11-SEP-2000; 2000JP-00274219.
 XX PA (WAKP) WAKO PURE CHEM IND LTD.
 XX PI Yamamoto S, Shiro M, Hanada T, Kobatake S;
 XX DR WPI; 2002-294073/34.
 XX PT Hybrid enzyme having a foreign peptide, useful for measuring
 PT macromolecule material in homogeneous system, has its activity modulated
 PT when a material capable of binding the peptide is introduced.
 XX PS Claim 17; Page 25-28; 74pp; English.
 XX CC The invention relates to a hybrid enzyme having a foreign peptide. The
 CC hybrid enzyme has an enzyme activity similar to that prior to the
 CC substitution or insertion of the peptide and having a property that the
 CC hybrid enzyme activity is modulated or modified when a material having
 CC binding ability to the peptide introduced by substitution or insertion is
 CC bound to the peptide moiety. The hybrid enzyme is useful for measuring C-
 CC reactive protein (CRP) by using an anti-CRP antibody in combination, and
 CC for measurement of a material containing the peptide introduced into the
 CC hybrid enzyme, or a material having binding ability to the peptide
 CC introduced into the hybrid enzyme. A recombinant DNA is useful for
 CC producing a protein having enzyme activity of G6PD, beta-galactosidase or
 CC alkaline phosphatase and a property that the enzyme is modulated when a
 CC material having binding ability to an amino acid sequence introduced into
 CC the enzyme by substitution or insertion is bound to the amino acid
 CC sequence, by culturing the transformant and collecting the protein. The
 CC hybrid enzyme is useful for both qualitative and quantitative analysis.
 CC The present sequence is Leucostoc mesenteroides glucose-6-phosphate
 CC dehydrogenase (G6PDH) used in the invention
 XX
 XX Sequence 486 AA;
 80
 Query Match 100.0%; Score 1516; DB 5; Length 486;
 Best Local Similarity 100.0%; Pred. No. 7.7e-131;
 Matches 294; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MVSEIKITLVTFPGGTGDLAKRKLTPSVNLTKKYLQGHFAIVGTARQALNDDEPKQLVR 60
 DB 1 MVSEIKITLVTFPGGTGDLAKRKLTPSVNLTKKYLQGHFAIVGTARQALNDDEPKQLVR 60
 QY 61 DSIDFTDDQAQAEAFIEHFSYRAHDVTDAAASYAVLKEAIEBAADKFDIDGNRIFYMSVA 120
 DB 61 DSIDFTDDQAQAEAFIEHFSYRAHDVTDAAASYAVLKEAIEBAADKFDIDGNRIFYMSVA 120
 QY 121 PRFFGTIAKYLKSEGLADTGVNRLMIKPEGTSYDTAAELQNDLENAFDDNQLFRIIDHY 180
 DB 121 PRFFGTIAKYLKSEGLADTGVNRLMIKPEGTSYDTAAELQNDLENAFDDNQLFRIIDHY 180
 QY 181 LGKEMVQNIALLRGNPIFDAAMNDYIKNOVTLSEVLGYEERAGYDTGALLDMTON 240
 DB 181 LGKEMVQNIALLRGNPIFDAAMNDYIKNOVTLSEVLGYEERAGYDTGALLDMTON 240
 QY 241 HTMOIVGWLAMEKPESTDKDIRAKNAAFNALKIYDEAEVVKYFVRAQYGAGD 294
 DB 241 HTMOIVGWLAMEKPESTDKDIRAKNAAFNALKIYDEAEVVKYFVRAQYGAGD 294